

```
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp Rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriophage:*
```

Pred. No. 18 is the number of results predicted by chance to have a greater than or equal score than the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	%			SUMMARIES			Description
	Score	Query Match	Length	DB	ID		
1	9	56.2	105	2	P96802	mycobacteri	P96802 mycobacteri
2	9	56.2	105	16	Q9CCQ8	mycobacteri	Q9CCQ8 mycobacteri
3	9	56.2	190	16	P71658		P71658 mycobacteri
4	9	56.2	406	10	Q94EV7	zea mays (m	Q94EV7 ze a mays (m
5	9	56.2	750	16	Q9KXP6	streptomyce	Q9KXP6 streptomyce
6	8	50.0	101	11	Q8BMY6	mus musculu	Q8BMY6 mus musculu
7	8	50.0	167	10	Q8SJ19	oryza sativ	Q8SJ19 oryza sativ
8	8	50.0	200	2	Q9X954		Q9X954
9	8	50.0	204	12	Q65545	bovine harp	Q65545 bovine harp
10	8	50.0	274	10	Q8S2E4		Q8S2E4
11	8	50.0	336	2	Q9XK0	pseudomonas	Q9XK0 pseudomonas
12	8	50.0	356	7	Q31191	muis musculu	Q31191 muis musculu
13	8	50.0	383	16	Q934A1		Q934A1 pseudomonas
14	8	50.0	451	10	Q8SJ12		Q8SJ12 oryza sativ
15	8	50.0	710	16	Q8TER0		Q8TER0 brucella mel
16	8	50.0	830	16	Q98C41		Q98C41 rhizobium l

				060961	leishmania
17	8	50.0	897	5	Q9S2X3 streptomyce
18	8	50.0	998	16	Q9S2K3 arabaena sp
19	7	43.8	69	16	Q8YUB7 salmonella
20	7	43.8	77	16	Q8Z3M8 escherichia
21	7	43.8	79	16	Q8FJU3 molluscum
22	7	43.8	109	12	Q11376 molluscum
23	7	43.8	110	12	Q98316 molluscum c
24	7	43.8	112	10	Q8H286 arabaena como
25	7	43.8	126	16	Q8KB54 chlorobium
26	7	43.8	132	16	Q8PP94 xanthomonas
27	7	43.8	157	4	Q8n9d2 homo sapiens
28	7	43.8	159	16	Q9I0C1 pseudomonas
29	7	43.8	161	4	Q8nh35 homo sapien
30	7	43.8	174	16	Q9a3R0 corynebacter
31	7	43.8	178	10	Q8LH12 coryza sativ
32	7	43.8	184	16	Q8FS32 corynebacte
33	7	43.8	188	2	Q9R6M4 agrobacteri
34	7	43.8	193	4	Q8WY44 ralstonia s
35	7	43.8	204	5	Q9U6W9 manduca sex
36	7	43.8	206	16	Q8PKQ0 xanthomonas
37	7	43.8	210	11	Q9D6J8 mus musculus
38	7	43.8	212	12	Q11344 methanobacter
39	7	43.8	227	16	Q8PRF8 xanthomonas
40	7	43.8	232	16	Q8XRQ0 ralstonia s
41	7	43.8	232	16	Q8FWQ1 brucella su
42	7	43.8	234	16	Q8f9g1 brucella su
43	7	43.8	251	10	Q8S6W0 oryza sativ
44	7	43.8	252	16	Q8YBm6 brucella me
45	7	43.8	264	10	Q94J70 oryza sativ
		43.8	276	16	Q8nm1 corynebacte

ALIGNMENT S

RESULT 1			
P96802		PRELIMINARY;	PRT; 105 AA.
ID P96802;			
AC P96802;			
DT 01-MAY-1997	(TREMBLrel.	03'	Created)
DT 01-MAY-1997	(TREMBLrel.	03'	Last sequence update)
DR 01-MAY-2001	(TREMBLrel.	19'	Last annotation update)
DE Integration host factor.			
GN Mycobacterium smegmatis.			
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetales;			
OC Corynebacteriales; Mycobacteriaceae; Mycobacterium.			
NCBI_TAXID=1772;			
OX			

Qy	7 AAARRAAE 15 	Preliminary	PRT;	105 AA.
Db	19 AAARRAAE 27			
RESULT 2				
Q9CCQ8	Q9CCQ8	PRELIMINARY;	PRT;	105 AA.
TD	AC			
DR	DR	01-JUN-2001 (TREMBUREL. 17, Created)		
DR	DR	01-JUN-2001 (TREMBUREL. 17, Last sequence update)		
DE	DE	01-OCT-2001 (TREMBUREL. 18, Last annotation update)		
DE	DE	Putative integration host factor.		
GN	GN	MTHF Q9 MR050		

DR	InterPro; IPR004507; Ubix.	Query Match	50.0%; score 8;	DB 10;	Length 274;
DR	Pfam; PF02441; Flavoprotein;	Best Local Similarity	100.0%;	Pred. No. 36;	Gaps 0;
DR	PFAMMS; TIGR0421; ubix; 1.	Matches	8;	Mismatches 0;	Indels 0;
SQ	SEQUENCE 200 AA; 21660 MW; .83D1B5C22C13CD3E CRC64;	Qy	7 AAARRARA 14		
Query Match	50.0%; score 8;	DB 2;	Length 200;		
Best Local Similarity	100.0%;	Pred. No. 28;			
Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;		
Oy	3 RAARAAAR 10	Gaps 0;			
Db	187 RAARAAAR 194				
RESULT 9					
ID Q65545	PRELIMINARY;	PRT;	204 AA.		
AC Q65545;					
DT 01-NOV-1996 (TREMBLrel. 01; Created)					
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)					
DE UL3 protein.					
GN					
OS Bovine herpesvirus 1.					
CC dsDNA viruses, no RNA stage. Herpesviridae;					
OC Alphaherpesvirinae; Varicellovirus.					
OX NCBI_TAXID=10320;					
RN [1]					
RP	SEQUENCE FROM N.A.				
RC STRAIN-COOPER;					
RX MEDLINE-96036477; PubMed-7483276;					
RA Khattar S.K., van Drunen Littel-van den Hurk S., Babiuuk L.A.,					
RA Tikoo S.R.;					
RT *Identification and transcriptional analysis of a 3'-coterminal gene cluster containing UL1, UL2, UL3, and UL3.5 open reading frames Of bovine herpesvirus 1.;					
RT Virology 213:128-137(1995).					
RL EMBL; U32173; AAC54557.1;					
DR InterPro; IPR005035; harpes_UL3.					
DR InterPro; IPR005822; sug_transporter..					
DR Pfam; PF03369; Herpes_UL3; 1.					
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.					
SQ SEQUENCE 204 AA; 21732 MW; .9232E6A8AA2CB8C6 CRC64;					
Query Match	50.0%; score 8;	DB 12;	Length 204;		
Best Local Similarity	100.0%;	Pred. No. 28;			
Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;		
Oy	3 RAARAAAR 10	Gaps 0;			
Db	113 RAARAAAR 120				
RESULT 10					
ID Q8GZEA	PRELIMINARY;	PRT;	274 AA.		
AC Q8GZEA;					
DT 01-MAR-2003 (TREMBLrel. 23; Created)					
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)					
DE Chlorophyll A-C binding protein.					
OS Pyrocystis lunula.					
OC Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.					
OX NCBI_TAXID=2972;					
RN [1]					
RP	SEQUENCE FROM N.A.				
RA Okamoto O.K., Hastings J.W.;					
RT "Circadian oscillations in the transcriptome of dinoflagellate cells: towards the clock circuitry."					
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases					
RL ENBL; AF508361; AAO1680_1;					
SEQUENCE 274 AA; 28168 MW; .B5F522A5D45AC8BA CRC64;					
SQ					

"Circadian oscillations in the transcriptome of dinoflagellate cells: towards the clock circuitry."

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases

SEQUENCE 274 AA; 28168 MW; .B5F522A5D45AC8BA CRC64;

Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565(1983).

FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

SEQUENCE FROM N.A.

RP MEDLINE-84170268; PubMed-6143316;

RA Lalanne J.-L., Cochet M., Kummer A.-M., Gachelin G., Kourilsky P.;

RT *Different exon-intron organization at the 5' part of a mouse class I gene is used to generate a novel H-2Kd-related mRNA.;

RT Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565(1983).

CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN) (BY SIMILARITY).

Sat Aug 9 19:18:32 2003

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Db 156 ARAAARR 163

Search completed: August 9, 2003, 16:32:58
Job time : 40.4571 secs